**Supporting Information**

*Mapping the Cytochrome* c *Folding Landscape*

Lyubovitsky, J. G.; Gray, H. B.; Winkler, J. R.

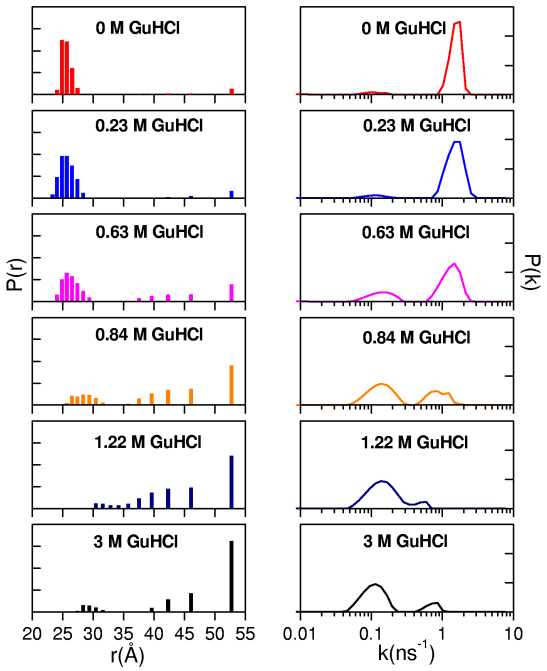


**Figure S1** GuHCl induced changes in the distributions of luminescence decay rates (*P(k)*, right) and ***D-A*** distances (*P(r)*, left) in DNS(C102)-cyt *c* (pH 7, 22 °C). Kinetics data fit using the ME algorithm.

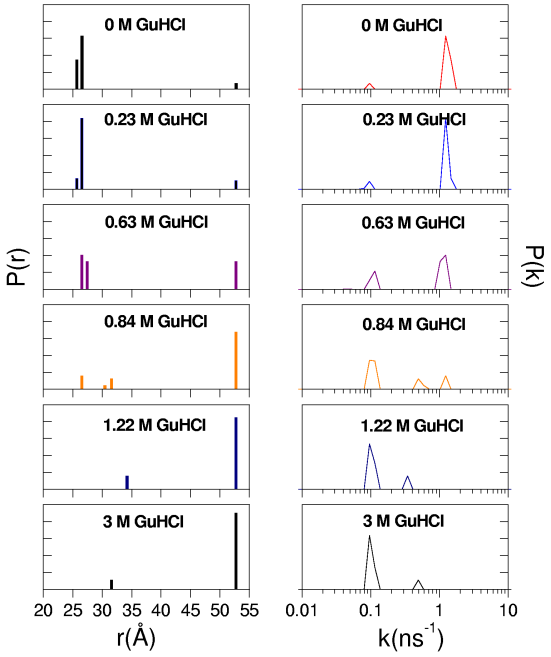


**Figure S2** GuHCl induced changes in the distributions of luminescence decay rates (*P(k)*, right) and ***D-A*** distances (*P(r)*, left) in DNS(C102)-cyt *c* (pH 7, 22 °C). Kinetics data fit using the LSQNONNEG algorithm.

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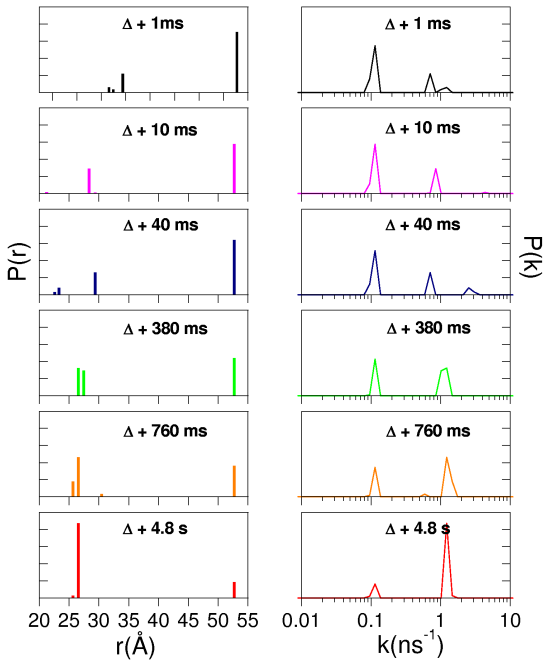


**Figure S3** Evolution of the distributions of luminescence decay rates (*P(k)*, right) and ***D-A*** distances (*P(r)*, left) during the refolding of DNS(C102)-cyt *c* ([GuHCl] = 0.13 M, pH 7, 22 °C). Kinetics data fit using the LSQNONNEG algorithm.

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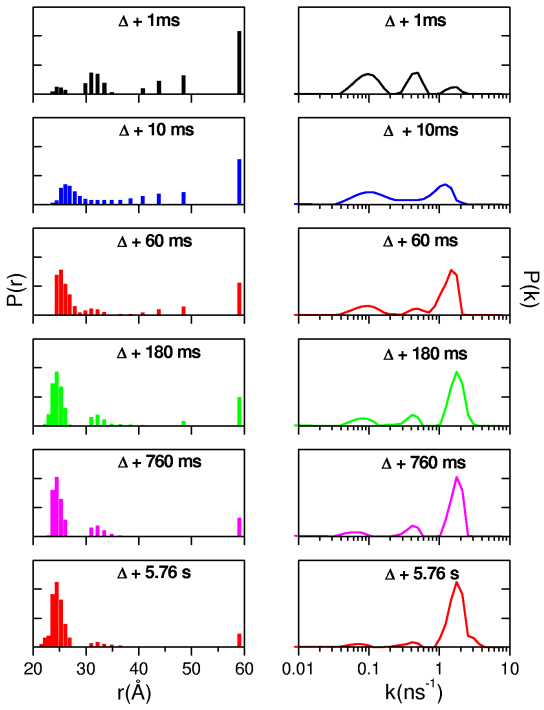


**Figure S4** Evolution of the distributions of luminescence decay rates (*P(k)*, right) and ***D-A*** distances (*P(r)*, left) during the refolding of DNS(C102)-cyt *c* in the presence of imidazole ([GuHCl] = 0.13 M, [im] = 0.15 M, pH 7, 1 °C). Kinetics data fit using the ME algorithm.

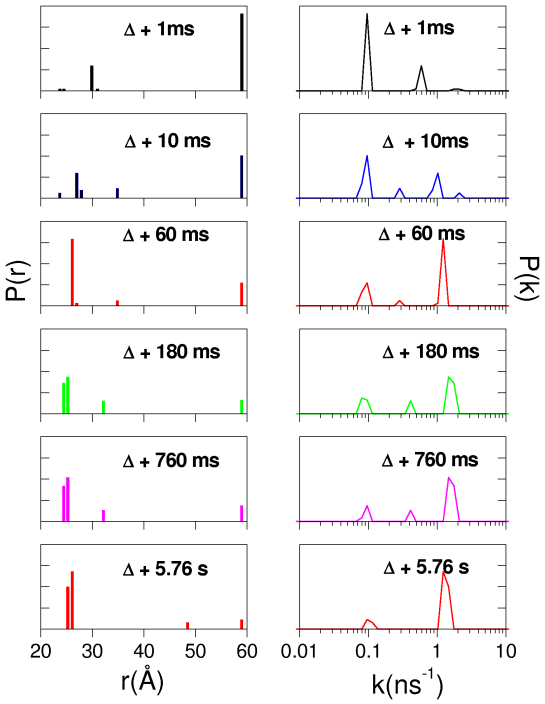


**Figure S5** Evolution of the distributions of luminescence decay rates (*P(k)*, right) and ***D-A*** distances (*P(r)*, left) during the refolding of DNS(C102)-cyt *c* in the presence of imidazole ([GuHCl] = 0.13 M, [im] = 0.15 M, pH 7, 1 °C). Kinetics data fit using the LSQNONNEG algorithm.